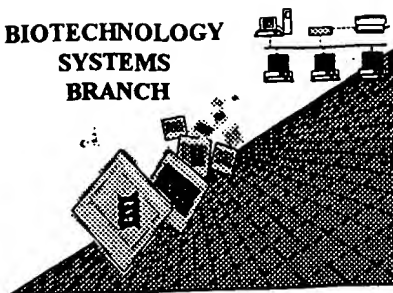


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



KW

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/856,796
Source: Per/09
Date Processed by STIC: 6/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

RAW SEQUENCE LISTING PATENT APPLICATION US/09/856,796

DATE: 07/06/2001
TIME: 04:30:40

INPUT SET: S36582.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

see item 4 on
Err summary
sheet

Does Not Comply
Corrected Diskette Needed

1 GENERAL INFORMATION: SEQUENCE LISTING

(1) General Information

(i) APPLICANT: DEPOSITOR:

move up - all responses must be on same line as heading
(A) NAME: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
(B) STREET: 3, rue Michel-Ange
(C) CITY: PARIS
(E) COUNTRY: FRANCE
(F) POSTAL CODE: 75794 CEDEX 16

delete

add these
MANDATORY
headings and
responses

(ii) TITLE OF THE INVENTION: NF-?B ACTIVATION INHIBITORS, AND THEIR PHARMACEUTICAL USES

(iii) NUMBER OF SEQUENCES: 4

(v) COMPUTER READABLE FORM:

MEDIUM TYPE 1
(A) TYPE OF SUPPORT: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) USER SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)

(vi) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(vii) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

add these mandatory headings

ERRORED SEQUENCES FOLLOW:

24 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs
(B) TYPE: nucleotide
(C) NUMBER OF STRANDS: double
(D) CONFIGURATION: linear

STRANDEDNESS:

(ii) TYPE OF MOLECULE: DNA (genomic)

MOLECULE TYPE 1

(ix) CHARACTERISTIC FEATURE:

(A) NAME/KEY: CDS
(B) POSITION: 1..609

*FYI: EPO
format is
invalid
for U.S.
cases*

*FYI: all U.S.
applications
which cannot claim
a prior application
filed before July 1, 1998,
must be in new sequence Rules
format.*

RAW SEQUENCE LISTING PATENT APPLICATION US/09/856,796

DATE: 07/06/2001
TIME: 04:30:40

INPUT SET: S36582.raw

```

--> 40      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
41
42      ATG GCT ACA GGC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG CTC
43      48
44      Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
45      1          5          10          15
46
47      TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT CCC TTA
48      96
49      Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
50      20          25          30
51
52      TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT CTG CAC CAG
53      144
54      Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu His Gln
55      35          40          45
56
57
58      CTG GCC TTT GAC ACC TAC CAG GAG TTT AAC CCC CAG ACC TCC CTC TGT
59      192
60      Leu Ala Phe Asp Thr Tyr Gln Glu Phe Asn Pro Gln Thr Ser Leu Cys
61      50          55          60
62
63      TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG GAG GAA ACA CAA CAG
64      240
65      Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln
66      65          70          75          80
67
68      AAA TCC AAC CTA GAG CTG CTC CGC ATC TCC CTG CTG CTC ATC CAG TCG
69      288
70      Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser
71      85          90          95
72
73      TGG CTG GAG CCC GTG CAG TTC CTC AGG AGT GTC TTC GCC AAC AGC CTG
74      336
75      Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu
76      100          105          110
77
78      GTG TAC GGC GCC TCT GAC AGC AAC GTC TAT GAC CTC CTA AAG GAC CTA
79      384
80      Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu
81      115          120          125
82
83      GAG GAA GGC ATC CAA ACG CTG ATG GGG AGG CTG GAA GAT GGC AGC CCC
84      432
85      Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro
86      130          135          140
87
88      CGG ACT GGG CAG ATC TTC AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC
89      480
90      Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn
91      145          150          155          160
92

```

48
(format
error)
(see item 1
on Error
summary
sheet)

RAW SEQUENCE LISTING PATENT APPLICATION US/09/856,796

 DATE: 07/06/2001
 TIME: 04:30:41

INPUT SET: S36582.raw

```

93  TCA CAC AAC GAT GAC GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC
94  528
95  Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys
96      165                      170                      175
97
98  TTC AGG AAG GAC ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG
99  576
100 Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln
101      180                      185                      190
102
103 TGC CGC TCT GTG GAG GGC AGC TGT GGC TTC TAG
104 609
105 Cys Arg Ser Val Glu Gly Ser Cys Gly Phe *
106      195                      200
107
108

```

 109 (2) INFORMATION FOR SEQ ID NO: 2:

110

111 (i) SEQUENCE CHARACTERISTICS:

112 (A) LENGTH: 202 amino acids

113 (B) TYPE: amino acid

 --> 114 (D) ~~CONFIGURATION~~: linear
115 *TOPOLOGY?*

116 (ii) MOLECULE TYPE: protein

--> 117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

118

119 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu Leu

120 1 5 10 15

121

122 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu

123 20 25 30

124

125 Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu His Gln

126 35 40 45

127

128 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Asn Pro Gln Thr Ser Leu Cys

129 50 55 60

130

131 Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln

132 65 70 75 80

133

134 Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser

135 85 90 95

136

137 Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu

138 100 105 110

139

140 Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu

141 115 120 125

142

143 Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro

144 130 135 140

RAW SEQUENCE LISTING PATENT APPLICATION US/09/856,796

DATE: 07/06/2001
TIME: 04:30:41

INPUT SET: S36582.raw

```

145
146 Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn
147 145 150 155 160
148
149 Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys
150 165 170 175
151
152 Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln
153 180 185 190
154
155 Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
156 195 200
157

```

158 (2) INFORMATION FOR SEQ ID NO: 3:

159

160 (i) SEQUENCE CHARACTERISTICS:

--> 161 (A) LENGTH: 581 ~~amino acids~~
 162 (B) TYPE: ~~nucleotide~~
 --> 163 (C) NUMBER OF STRANDS: double
 --> 164 (D) CONFIGURATION: linear

fix these headings

165

166 (ii) MOLECULE TYPE: DNA (genomic)

167

168

--> 169 (ix) CHARACTERISTIC

--> 170 (A) NAME/KEY: CDS
 --> 171 (B) POSITION: 1..582

fix this

172

173

--> 174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

175

176 ATG GGG GTG CAC GAA TGT CCT GCC TGG CTG TGG CTT CTC CTG TCC CTG

177 48

178 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu

179 205 210 215

180

181 CTG TCG CTC CCT CTG GGC CTC CCA GTC CTG GGC GCC CCA CCA CGC CTC

182 96

183 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu

184 220 225 230 235

185

186 ATC TGT GAC AGC CGA GTC CTG GAG AGG TAC CTC TTG GAG GCC AAG GAG

187 144

188 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu

189 240 245 250

190

191 GCC GAG AAT ATC ACG ACG GGC TGT GCT GAA CAC TGC AGC TTG AAT GAG

192 192

193 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu

194 255 260 265

195

196 AAT ATC ACT GTC CCA GAC ACC AAA GTT AAT TTC TAT GCC TGG AAG AGG

48
format over

RAW SEQUENCE LISTING PATENT APPLICATION US/09/856,796

DATE: 07/06/2001
TIME: 04:30:41

INPUT SET: S36582.raw

```

197 240
198 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
199      270      275      280
200
201 ATG GAG GTC GGG CAG CAG GCC GTA GAA GTC TGG CAG GGC CTG GCC CTG
202 288
203 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
204      285      290      295
205
206 CTG TCG GAA GCT GTC CTG CGG GGC CAG GCC CTG TTG GTC AAC TCT TCC
207 336
208 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
209 300      305      310      315
210
211 CAG CCG TGG GAG CCC CTG CAG CTG CAT GTG GAT AAA GCC GTC AGT GGC
212 384
213 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
214      320      325      330
215
216 CTT CGC AGC CTC ACC ACT CTG CTT CGG GCT CTG GGA GCC CAG AAG GAA
217 432
218 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
219      335      340      345
220
221 GCC ATC TCC CCT CCA GAT GCG GCC TCA GCT GCT CCA CTC CGA ACA ATC
222 480
223 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
224      350      355      360
225
226 ACT GCT GAC ACT TTC CGC AAA CTC TTC CGA GTC TAC TCC AAT TTC CTC
227 528
228 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
229      365      370      375
230
231 CGG GGA AAG CTG AAG CTG TAC ACA GGG GAG GCC TGC AGG ACA GGG GAC
232 576
233 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
234 380      385      390      395
235
236 AGA TGA
237 582
238 Arg
239
240
241

```

*same
even*

242 (2) INFORMATION FOR SEQ ID NO: 4:

243

244 (i) SEQUENCE CHARACTERISTICS:

245 (A) LENGTH: 193 amino acids

246 (B) TYPE: amino acid

247 (D) CONFIGURATION: linear

248

-->

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/09/856,796

DATE: 07/06/2001
TIME: 04:30:42

INPUT SET: S36582.raw

Line	Error	Original Text
5	Unknown or Misplaced Identifier	(i) DEPOSITOR:
6	Unknown or Misplaced Identifier	(A) NAME: CENTRE NATIONAL DE LA RECHERCHE
7	Unknown or Misplaced Identifier	(B) STREET: 3, rue Michel-Ange
8	Unknown or Misplaced Identifier	(C) CITY: PARIS
9	Unknown or Misplaced Identifier	(E) COUNTRY: FRANCE
10	Unknown or Misplaced Identifier	(F) POSTAL CODE: 75794 CEDEX 16
18	Unknown or Misplaced Identifier	(A) TYPE OF SUPPORT: Floppy disk
20	Unknown or Misplaced Identifier	(C) USER SYSTEM: PC-DOS/MS-DOS
27	Entered (609) and Calc. Seq. Length (0) differ	(A) LENGTH: 609 base pairs
29	Unknown or Misplaced Identifier	(C) NUMBER OF STRANDS: double
30	Unknown or Misplaced Identifier	(D) CONFIGURATION: linear
32	Unknown or Misplaced Identifier	(ii) TYPE OF MOLECULE: DNA(genomic)
35	Unknown or Misplaced Identifier	(ix) CHARACTERISTIC:
36	Unknown or Misplaced Identifier	(A) NAME/KEY: CDS
37	Unknown or Misplaced Identifier	(B) POSITION: 1..609
40	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
40	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
114	Unknown or Misplaced Identifier	(D) CONFIGURATION: linear
117	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
158	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO: 3:
161	Entered (582) and Calc. Seq. Length (0) differ	(A) LENGTH: 582 base pairs
163	Unknown or Misplaced Identifier	(C) NUMBER OF STRANDS: double
164	Unknown or Misplaced Identifier	(D) CONFIGURATION: linear
169	Unknown or Misplaced Identifier	(ix) CHARACTERISTIC:
170	Unknown or Misplaced Identifier	(A) NAME/KEY: CDS
171	Unknown or Misplaced Identifier	(B) POSITION: 1..582
174	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
174	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
247	Unknown or Misplaced Identifier	(D) CONFIGURATION: linear
249	Unknown or Misplaced Identifier	(ii) TYPE OF MOLECULE: protein
250	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
295	Stop Codon at end of sequence removed - no error	

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/856,796

DATE: 07/06/2001
TIME: 04:30:42

INPUT SET: S36582.raw

APPLICANT
ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
MEDIUM TYPE
OPERATING SYSTEM
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA
STRANDEDNESS
TOPOLOGY

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/856,796DATE: 07/06/2001
TIME: 04:30:42

INPUT SET: S36582.raw

--> 249 (ii) TYPE OF MOLECULE protein
--> 250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

251
252 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
253 1 5 10 15
254
255 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
256 20 25 30
257
258 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
259 35 40 45
260
261 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
262 50 55 60
263
264 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
265 65 70 75 80
266
267 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
268 85 90 95
269
270 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
271 100 105 110
272
273 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
274 115 120 125
275
276 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
277 130 135 140
278
279 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
280 145 150 155 160
281
282 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
283 165 170 175
284
285 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
286 180 185 190
287
288 Arg
289
290
291
292
293
294
295 1 delete
296
297
298
299

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/886,796

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.